

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 17:57:00 ; Search time 2667.65 Seconds
(without alignments)
4064.586 Million cell updates/sec

Title: US-09-784-340-3_COPY_7800_8500
Perfect score: 701
Sequence: 1 gttgtgtcaagtacgagaaa.....taggattccagaaaatta 701

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
6: gb_in3:*
7: gb_om:*
8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_pi1:*
12: gb_pi2:*
13: gb_pi3:*
14: gb_pi4:*
15: gb_pi5:*
16: em_ba1:*
17: em_ba2:*
18: em_fun:*
19: em_htgo_hum:*
20: em_htgo_inv:*
21: em_htgo_rod:*
22: em_htgo_hum1:*
23: em_htgo_hum2:*
24: em_htgo_hum3:*
25: em_htgo_hum4:*
26: em_htgo_hum5:*
27: em_htgo_hum6:*
28: em_htgo_hum7:*
29: em_htgo_hum8:*
30: em_htg_inv1:*
31: em_htg_inv2:*
32: em_htg_other:*
33: em_htg_rod:*
34: em_hum1:*
35: em_hum2:*
36: em_hum3:*
37: em_hum4:*
38: em_hum5:*
39: em_hum6:*
40: em_hum7:*
41: em_in:*
42: em_om:*
43: em_or:*

44: em_ov:*
45: em_pat:*
46: em_ph:*
47: em_pi:*
48: em_ro:*
49: em_sts:*
50: em_sy:*
51: em_un:*
52: em_v1:*
53: gb_sts1:*
54: gb_sts2:*
55: gb_sts3:*
56: gb_sy:*
57: gb_un:*
58: gb_v11:*
59: gb_v12:*
60: gb_htg1:*
61: gb_htg2:*
62: gb_htg3:*
63: gb_htg4:*
64: gb_htg5:*
65: gb_htg6:*
66: gb_htg7:*
67: gb_htg8:*
68: gb_htg9:*
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70: gb_htg11:*
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82: gb_htg23:*
83: gb_htg24:*
84: gb_htg25:*
85: gb_pi1:*
86: gb_pi2:*
87: gb_pi3:*
88: gb_pi4:*
89: gb_pi5:*
90: gb_pi6:*
91: gb_pi7:*
92: gb_pi8:*
93: gb_pi9:*
94: gb_pi10:*
95: gb_pi11:*
96: gb_pi12:*
97: gb_pi13:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	701	100.0	212904	66	AC021146	AC021146 Homo sapi
C 2	194	27.7	135350	81	AL391626	AL391626 Homo sapi
C 3	185.2	26.4	174437	60	AC007768	AC007768 Homo sapi
C 4	185.2	26.4	199702	77	AC087178	AC087178 Homo sapi
C 5	183.6	26.2	151628	64	AC016665	AC016665 Homo sapi
C 6	183.6	26.2	151874	62	AC011268	AC011268 Homo sapi
C 7	183.6	26.2	187889	65	AC019306	AC019306 Homo sapi
C 8	180.8	25.8	159930	78	AL138757	AL138757 Homo sapi

9	180.6	25.8	107484	92	HS424L16	AL034373	Human	DNA
10	180.6	25.8	168224	67	AC022976	AC022976	Homo sapi	
11	180.4	25.7	180442	71	AC068599	AC068599	Homo sapi	
12	179.4	25.6	151560	73	AC036223	AC036223	Homo sapi	
13	179.4	25.6	153038	64	AC016873	AC016873	Homo sapi	
14	178.2	25.4	176748	81	AL513493	AL513493	Homo sapi	
15	177.2	25.3	168041	75	AC073874	AC073874	Homo sapi	
16	172	24.5	186343	89	AL137248	AL137248	Human	DNA
17	172	24.5	196966	71	AC031975	AC031975	Homo sapi	
18	170.8	24.4	157367	77	AC084769	AC084769	Homo sapi	
19	170.4	24.3	180095	72	AL355507	AL355507	Homo sapi	
20	169.6	24.2	137730	92	HS365E2	AL009177	Human	DNA
21	167.6	23.9	161665	76	AC084032	AC084032	Homo sapi	
22	167.6	23.9	163120	62	AC012480	AC012480	Homo sapi	
23	166.6	23.8	169653	82	AL445430	AL445430	Homo sapi	
24	165	23.5	116841	82	AP000643	AP000643	Homo sapi	
25	165	23.5	167639	91	AP001827	AP001827	Homo sapi	
26	164.8	23.5	154268	80	AL356463	AL356463	Homo sapi	
27	164.8	23.5	157122	69	AC026235	AC026235	Homo sapi	
28	163.4	23.3	186266	91	AL512782	AL512782	Human	DNA
29	162.8	23.2	162493	75	AC073972	AC073972	Homo sapi	
30	160.8	22.9	169013	92	HS138A5	AC044813	Human	DNA
31	159.8	22.8	188351	71	AC044813	AC044813	Homo sapi	
32	158	22.5	207320	63	AC012656	AC012656	Homo sapi	
33	157.6	22.5	202793	91	CNS06C83	AL391158	Human	chr
34	157.4	22.5	184042	87	AC011235	AC011235	Homo sapi	
35	156.6	22.3	148454	86	AC007023	AC007023	Homo sapi	
36	156.4	22.3	146903	68	AC024410	AC024410	Homo sapi	
37	155	22.1	142693	62	AC012032	AC012032	Homo sapi	
38	154.8	22.1	132614	70	AC026772	AC026772	Homo sapi	
39	154.8	22.1	178340	67	AC022120	AC022120	Homo sapi	
40	154.8	22.1	198896	60	AC008638	AC008638	Homo sapi	
41	154	22.0	107587	78	AL139416	AL139416	Homo sapi	
42	154	22.0	142069	90	AL445991	AL445991	Human	DNA
43	153.6	21.9	170117	79	AL158827	AL158827	Homo sapi	
44	153.6	21.9	171575	64	AC015926	AC015926	Homo sapi	
45	153.6	21.9	182288	82	AL589843	AL589843	Homo sapi	

ALIGNMENTS

RESULT 1
AC021146/c HTG 07-JUL-2000
LOCUS Homo sapiens chromosome 4 clone RP11-468M14, WORKING DRAFT
DEFINITION
AC021146 212904 bp DNA
AC021146 SEQUENCE, 24 unordered pieces.
AC021146.4 GI:8568861
AC021146.4 HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
On Jun 16, 2000 this sequence version replaced gl:7344259.

FEATURES

source

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H_NH0468N14
Summary Statistics

Sequencing vector: M13: 88%
Sequencing vector: plasmid: 12%
Chemistry: Dye-primer ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990.19
Consensus quality: 199729 bases at least Q40
Consensus quality: 203731 bases at least Q30
Consensus quality: 206340 bases at least Q20
Insert size: 215000; agarose-fp
Insert size: 210604; sum-of-contigs
Quality coverage: 3.75 in Q20 bases; sum-of-contigs
Quality coverage: 3.83 in Q20 bases; sum-of-contigs
NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1564: contig of 1564 bp in length
1565: gap of unknown length
1665: contig of 1421 bp in length
3086: gap of unknown length
3186: contig of 1949 bp in length
5135: gap of unknown length
5235: contig of 2935 bp in length
8170: gap of unknown length
8270: contig of 2072 bp in length
10341: contig of 3512 bp in length
10441: gap of unknown length
13614: contig of 3173 bp in length
13714: gap of unknown length
13715: gap of 3375 bp in length
13715: contig of 3375 bp in length
17189: gap of unknown length
17190: contig of 3512 bp in length
20701: gap of unknown length
20801: gap of unknown length
25001: contig of 4200 bp in length
25002: gap of unknown length
25101: gap of 3919 bp in length
25102: contig of 3919 bp in length
28021: gap of unknown length
29120: gap of 4236 bp in length
29121: contig of 4236 bp in length
33356: gap of unknown length
33357: gap of 3446 bp in length
33457: contig of 3446 bp in length
36903: gap of unknown length
37002: gap of 5973 bp in length
42975: contig of 5973 bp in length
43075: gap of unknown length
48339: gap of 5264 bp in length
48340: contig of 5264 bp in length
48439: gap of unknown length
56529: contig of 8090 bp in length
56530: gap of unknown length
56530: gap of unknown length
65313: contig of 8584 bp in length
65314: gap of unknown length
65314: gap of 9402 bp in length
74715: contig of 9402 bp in length
74716: gap of unknown length
74816: contig of 13731 bp in length
88546: gap of unknown length
88547: gap of 14721 bp in length
103367: contig of 14721 bp in length
103368: gap of unknown length
103468: contig of 14700 bp in length
118167: gap of unknown length
118168: gap of unknown length
118267: gap of unknown length
118268: contig of 14498 bp in length
132766: gap of unknown length
132865: gap of 21227 bp in length
154092: contig of 21227 bp in length
154192: gap of unknown length
154193: gap of unknown length
182145: contig of 27952 bp in length
182145: gap of unknown length
212904: contig of 30660 bp in length.
Location/Qualifiers
1. 212904
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"

BASE COUNT 69110 a 36915 c 37432 g 67121 t 2326 others
ORIGIN

/clone="RP11-468N14"
Query Match 100.0%; Score 701; DB 66; Length 212904;
Best Local Similarity 100.0%; Pred. No. 7.6e-159;
Matches 701; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gttgttgtaagtgagaaacatggtgggaacttaaccacacataataataacagaac 60
|||||
DB 79805 GTCTGTGTCAGTGAGAAAACATGGAGAACTTAACCAACATAAAATAACAGAAC 79746
OY 61 agcttccttgaccattctcagagaaagtgtaacatcccttgtaagccactagaa 120
|||||
DB 79745 AGCTTCTTTCACCATTTCTAGAGAAAAGAGTTCAGCATCCCTTGTAGGCCACTAGAA 79686
OY 121 gaagaaatctctcgggaaagacatcaaccaatgaaatgagaccagaagagatg 180
|||||
DB 79685 GAAGAAATCTCTGGGAAAAGCAGATTCACCAATGAATGAGACCAGAAAGAGATG 79626
OY 181 agggactatgtgccaaaatgtaactgggataccaggtgttaactagtgggttccaa 240
|||||
DB 79625 AGGATCTATGTGCCAAAATGTTAACTGGGATCCAGGCTGTACTAGGCGTTCCAA 79566
OY 241 tggggagactgtaattgtaggttaatgcaagcagagcaaaagtcactggagactctg 300
|||||
DB 79565 TGGGGAACGTATATTGTGTAGGTTAATGCAAGAGCAGCAAAAGTCCATGAGGCATTCTG 79506
OY 301 agactgaaagatagtcaactttgacatactgcacagaatctgactgataccaagcca 360
|||||
DB 79505 AGACTGAAGATAGTCACTTGGCATATTCGACAGAAATCGATGATGATGATCAAGCCA 79446
OY 361 agtagctgtatctagtgtccctaataggtgtgtaccagagcagtggttaagtaaaa 420
|||||
DB 79445 AGTAGGCTGTATGTAGTGTGCTATAGGGGTGTACCAAGAGCAGAGTGTGTAGTAAAA 79386
OY 421 tctgtactgacacatctgaaggaatggaagagtgtaagactttaacggtctcagtt 480
|||||
DB 79385 TCTGTACTGACACATTTGAGAGAAATGGAAGAGAGTGAAGATTTTAAACCGTCTACTGT 79326
OY 481 tgaataagactgtctctgtgtaagaaatcaactatataatttaaatgcatagccagac 540
|||||
DB 79325 TGACTGAAGACCTCTCTGTGTATGAAAAATTAATATTTTAAATGATGATGCCAGAC 79266
OY 541 aaataataatataaagaattaccacaatagctatgtaacaaactggttactact 600
|||||
DB 79265 AACATAAATTAATAAATTTACACAAATGATGATGATGATGATGATGATGATGAT 79206
OY 601 actaagagtgtaaaagaaacccctcattccatttaagaaataatacaaatccca 660
|||||
DB 79205 ACTACAGAGGAGAAAAGAAACCTCTCATTTTCCATTTTATGGAATATAATCAAAATCTTA 79146
OY 661 taaggaagtttcagagccagtaggatttcagaaaaaatta 701
|||||
DB 79145 TAAGGAAGTTTCAGAGCCAGTAGATTTCCAGAAAAATTA 79105

RESULT 2
AL391626/c DNA HTG 20-JAN-2001
LOCUS AL391626/c
DEFINITION Homo sapiens chromosome 1 clone RP11-202K23, *** SEQUENCING IN
PROGRESS ***, 21 unordered pieces.
ACCESSION AL391626
VERSION AL391626.1 GI:9931033
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 135350)
AUTHORS Plumb,B.
TITLE Direct Submission

JOURNAL COMMENT

Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonequest@sanger.ac.uk
Genome Center

Center: Sanger Centre
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

Project Information
Center project name: BA202K23

Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 10% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 126914 bases at least Q40
Consensus quality: 130362 bases at least Q30
Consensus quality: 131723 bases at least Q20
Insert size: 13350; sum-of-contigs
Insert size: 144571; 2.1% error; again: 3-fp
Quality coverage: 3.68x in Q20 bases; sum-of-contigs
Quality coverage: 3.46x in Q20 bases; agarose p

NOTE: This is a 'working draft' sequence. It currently
consists of 21 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1 3427: contig of 3427 bp in length
3428 3527: gap of 100 bp
3528 11200: contig of 7673 bp in length
11201 11300: gap of 100 bp
11301 14155: contig of 2855 bp in length
14156 14255: gap of 100 bp
14256 31692: contig of 17437 bp in length
31693 31792: gap of 100 bp
31793 34235: contig of 2443 bp in length
34236 34335: gap of 100 bp
34336 38905: contig of 4570 bp in length
38906 39005: gap of 100 bp
39006 43252: contig of 4247 bp in length
43253 43352: gap of 100 bp
43353 46981: contig of 3629 bp in length
46982 47081: gap of 100 bp
47082 51380: contig of 4299 bp in length
51381 51480: gap of 100 bp
51481 59247: contig of 7767 bp in length
59248 59347: gap of 100 bp
59348 66869: contig of 7522 bp in length
66870 66969: gap of 100 bp
66970 84168: contig of 17199 bp in length
84169 84268: gap of 100 bp
84269 98434: contig of 14166 bp in length
98435 98534: gap of 100 bp
98535 102586: contig of 4052 bp in length
102587 102686: gap of 100 bp
102687 105415: contig of 2729 bp in length
105416 105515: gap of 100 bp
105516 109302: contig of 3787 bp in length
109303 109402: gap of 100 bp
109403 112678: contig of 3276 bp in length
112679 112778: gap of 100 bp
112779 117961: contig of 5183 bp in length
117962 118061: gap of 100 bp
118062 128651: contig of 10590 bp in length
128652 128751: gap of 100 bp
128752 131919: contig of 3168 bp in length
131920 132019: gap of 100 bp
132020 135350: contig of 3331 bp in length.
Location/Qualifiers
1. 135350

FEATURES
SOURCE

```

/misc_feature /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-202K23"
/clone_id="RPOT-11.1"
1..3427
/note="assembly_fragment:00197
fragment_chain:1
clone_end:77
vector_side:left"
misc_feature 3528..11200
/note="assembly_fragment:00427
fragment_chain:1"
misc_feature 11301..14135
/note="assembly_fragment:00358
fragment_chain:1"
misc_feature 14256..31692
/note="assembly_fragment:00328
fragment_chain:1"
misc_feature 31793..34235
/note="assembly_fragment:00316
fragment_chain:1"
misc_feature 34336..38905
/note="assembly_fragment:00984
fragment_chain:1"
misc_feature 39006..43252
/note="assembly_fragment:00304
fragment_chain:2"
misc_feature 43353..46981
/note="assembly_fragment:00044
fragment_chain:2"
misc_feature 47082..51380
/note="assembly_fragment:00086
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misc_feature 51481..59247
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misc_feature 59348..66869
/note="assembly_fragment:00672
fragment_chain:3"
misc_feature 66970..84168
/note="assembly_fragment:00176
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misc_feature 84269..98434
/note="assembly_fragment:00450
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/note="assembly_fragment:00263
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misc_feature 102687..105415
/note="assembly_fragment:00058
fragment_chain:4"
misc_feature 105516..109302
/note="assembly_fragment:00846
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misc_feature 109403..112678
/note="assembly_fragment:01261
fragment_chain:4"
misc_feature 112779..117961
/note="assembly_fragment:00075
fragment_chain:4"
misc_feature 118062..128651
/note="assembly_fragment:00056
fragment_chain:4"
misc_feature 128752..131919
/note="assembly_fragment:01019
fragment_chain:4"
misc_feature 132020..135350
/note="assembly_fragment:00544
fragment_chain:4
clone_end:Spe
vector_side:right"
BASE COUNT 42934 a 23309 c 22268 g 44830 t 2009 others

```

```

ORIGIN
Query Match 27.7%; Score 194; DB: 135350;
Best Local Similarity 64.0%; Pred. No. 1.3e-14;
Matches 379; Conservative 0; Mismatches 5; Indels 18; Gaps 5;

QY 1 ggtgtgtcaagtgtgaaacatcgtgagaacttaccacacacataaatacaagaac 60
DB 86551 GTGTGGTCAGATGATGATACATAGAGCAACTCATATTAACACATTAATGACAGCAAGC 86492
QY 61 agtctcttgaccattct-agagaaagggttcagcatccctgttaaggccactagg 119
DB 86491 AGTTATGACATACAGGCTGTGAGAGAAACAGAGACACCTTTGGCGGTTAATGCGA 86432
QY 120 agaagaaattctctgtggaagaacacatcaaccaaataagagagacaaagaagagt 179
DB 86431 AGTGGAGGCCATCTTGGACATATGATCAATCAGTAGAGGAGCAAG-AGAGAGA 86374
QY 180 gagggatctatgtgccaagttaactgtgagatccagggtgttacctagtggtttcca 239
DB 86373 GGGGTCCTGTGACCCAAAGCCTTACTGSGGTCCAGGCGATATGACAGAGTTTCTT 86314
QY 240 atgggaactgtaatgtgttaagtttaatgaacagcagcacaagtcacatgagagcattct 299
DB 86313 GCAGGAGTTTAAATGTTAGAGTTAGACAAAGACATGCTCCATGAGCAGGCT 86254
QY 300 gagactgaaagtagtaccttggtcatatctgcacagaatctgcagtgatt----- 352
DB 86253 GTGACTGAGAGGTGTGCTCATGATATTTGACCTCCATGAGGAGATGATATCAATG 86194
QY 353 --caagccaaagtgtgtatctatgtgtccata-----ygtgtgtaccagaaggaca 405
DB 86193 GCACAGTCCATGAGTTTATCTATGCTGTCCAGTAAGAAAGTGTCACAGAGAGA 86134
QY 406 gtgtgtaagtaaaatcctgtcgtgaacacattgaggaatgaaaggaggtgaaatttt 465
DB 86133 GATGCACAGAAATAATGTGATTTGACACATGAGAACTGAGAGAGCAGCAAAAAATAG 86074
QY 466 aaaggtgtcagtggtgttaagacgtgtctgtgtatgaaatcaactatattt 524
DB 86073 AAACGTGTCAAAAGGTGACCATACCTTCTTGTAAGAGACAGTCCAGCATATTTA 86014
QY 525 aatgtcatgaccagacacataaaattataagaattaccacaatagtctatg 576
DB 86013 AATGTGATCTGTGAGCAATATAATTTAAGATTTGCTGCTGCTGATG 85962

RESULT 3
AC007768 174437 bp DNA HTG 20-APR-2000
LOCUS Homo sapiens chromosome 18 clone RP11-540M4 map 18, WORKING DRAFT
DEFINITION
ACCESSION AC007768.2 GI:7622399
VERSION AC007768
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 174437)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11:540M4
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 174437)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baker,J., Balow,J., Baines,N., Beckwith,R., Benn,J., Brown,A.,
Castle,A., Cerny,J., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearlano,K., Depayre,E., Dewar,K., Dewart,K.,
Donlan,L., Doyle,M., Ferreira,P., Fitzhugh,M., Forrest,C.,
Funke,R., Gage,D., Galagan,J., Gardina,S., Gilbert,D., Grant,G.,
Hagob,B., Heathford,A., Horton,L., Howland,J.C., Jones,C., Kahn,L.,
Karalas,A., Lenockky,J., Lieu,C., Locke,K., Macdonald,P.,

```

SEQUENCE, 41 unordered pieces.	
AC087178	
AC087178.2	GI:12204333
ACCESSION	
VERSION	

```

SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
TITLE       1 (bases 1 to 199702)
JOURNAL     Waterston, R.H.
REFERENCE   The sequence of Homo sapiens clone
AUTHORS     Unpublished
TITLE       2 (bases 1 to 199702)
JOURNAL     Waterston, R.H.
REFERENCE   Direct Submission
AUTHORS     Submitted (11-DEC-2000) Genome Sequencing Center, Washington
TITLE       University School of Medicine, 4444 Forest Park Parkway, St. Louis,
JOURNAL     MO 63108, USA
COMMENT     On Jan 13, 2001 this sequence version replaced gi:11612642.

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H_NH0793A13
----- Summary Statistics -----
Sequencing vector: M13; 100%
Sequencing vector: Plasmid; 0%
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 174880 bases at least Q40
Consensus quality: 182504 bases at least Q30
Consensus quality: 186170 bases at least Q20
Insert size: 199000; agarose-fp
Insert size: 194009; sum-of-contigs
Quality coverage: 2.87 in Q20 bases; agarose-fp
Quality coverage: 3.01 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 41 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
-----
1      1267: contig of 1267 bp in length
*      1368      1367: gap of unknown length
*      1368      2400: contig of 1033 bp in length
*      2401      2500: gap of unknown length
*      2501      4656: contig of 2156 bp in length
*      4657      4756: gap of unknown length
*      4757      6882: contig of 2126 bp in length
*      6883      6882: gap of unknown length
*      6983      8935: contig of 1953 bp in length
*      8936      9035: gap of unknown length
*      9036      11452: contig of 2417 bp in length
*      11453      11552: gap of unknown length
*      11553      13771: contig of 2219 bp in length
*      13772      13871: gap of unknown length
*      13872      15887: contig of 1716 bp in length
*      15888      15687: gap of unknown length
*      15688      19023: contig of 3336 bp in length
*      19024      19123: gap of unknown length
*      19124      22249: contig of 3126 bp in length
*      22250      22349: gap of unknown length
*      22350      24092: contig of 1743 bp in length
*      24093      24192: gap of unknown length
*      24193      26788: contig of 2596 bp in length
*      26789      26888: gap of unknown length
*      26889      30112: contig of 3224 bp in length
*      30113      30212: gap of unknown length
*      30213      32726: contig of 2514 bp in length
*      32727      32826: gap of unknown length
*      32827      36374: contig of 3548 bp in length

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*      36375      36474: gap of unknown length
*      36475      39233: contig of 2759 bp in length
*      39234      39333: gap of unknown length
*      39334      42723: contig of 3350 bp in length
*      42724      42823: gap of unknown length
*      42824      45983: contig of 3160 bp in length
*      45984      46083: gap of unknown length
*      46084      48934: contig of 2851 bp in length
*      48935      49034: gap of unknown length
*      49035      54923: contig of 5869 bp in length
*      49036      55023: gap of unknown length
*      55024      59263: contig of 4240 bp in length
*      59264      59363: gap of unknown length
*      59364      63218: contig of 3855 bp in length
*      63219      63318: gap of unknown length
*      63319      67133: contig of 3815 bp in length
*      67134      67233: gap of unknown length
*      67234      72233: contig of 5000 bp in length
*      72234      72333: gap of unknown length
*      72334      79233: contig of 6900 bp in length
*      79234      79333: gap of unknown length
*      79334      86110: contig of 6777 bp in length
*      86111      86210: gap of unknown length
*      86211      92685: contig of 6475 bp in length
*      92686      92785: gap of unknown length
*      92786      98826: contig of 6041 bp in length
*      98827      98926: gap of unknown length
*      98927      105081: contig of 6135 bp in length
*      105082      105181: gap of unknown length
*      105182      110628: contig of 5447 bp in length
*      110629      110728: gap of unknown length
*      110729      118730: contig of 8002 bp in length
*      118731      118830: gap of unknown length
*      118831      126388: contig of 7558 bp in length
*      126389      126488: gap of unknown length
*      126489      134257: contig of 7759 bp in length
*      134258      134357: gap of unknown length
*      134359      141443: contig of 7066 bp in length
*      141444      141543: gap of unknown length
*      141544      150881: contig of 9338 bp in length
*      150882      150981: gap of unknown length
*      150982      160811: contig of 9830 bp in length
*      160812      160911: gap of unknown length
*      160912      170464: contig of 9553 bp in length
*      170465      170564: gap of unknown length
*      170565      184947: contig of 14383 bp in length
*      184948      185047: gap of unknown length
*      185049      197809: contig of 12762 bp in length
*      197810      197909: gap of unknown length
*      197910      199041: contig of 1132 bp in length
*      199042      199141: gap of unknown length
*      199142      199702: contig of 561 bp in length.

FEATURES
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="RP11-793A13"
            /clone="RP11-793A13"
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        1368..2400
            /note="assembly_name:Contig13"
        2501..4656
            /note="assembly_name:Contig14"
        4757..6882
            /note="assembly_name:Contig15"
        6983..8935
            /note="assembly_name:Contig16"
        9036..11452
            /note="assembly_name:Contig17"
        11553..13771
            /note="assembly_name:Contig18"
        13872..15587

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15688. 19023
/note="assembly_name:Config20"
misc_feature /note="assembly_name:Config21"
19124. 22249
/note="assembly_name:Config22"
misc_feature /note="assembly_name:Config22"
22350. 24092
24193. 26788
/note="assembly_name:Config23"
misc_feature /note="assembly_name:Config24"
26889. 30112
30213. 32726
/note="assembly_name:Config25"
misc_feature /note="assembly_name:Config25"
32827. 36374
36475. 39233
/note="assembly_name:Config26"
misc_feature /note="assembly_name:Config27"
39334. 42723
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42824. 45983
46084. 48934
/note="assembly_name:Config29"
misc_feature /note="assembly_name:Config30"
49035. 54923
55024. 59263
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misc_feature /note="assembly_name:Config32"
59364. 63218
63319. 67133
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misc_feature /note="assembly_name:Config34"
67234. 72233
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misc_feature /note="assembly_name:Config36"
79334. 86110
86211. 92685
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misc_feature /note="assembly_name:Config38"
92786. 98826
98927. 105081
/note="assembly_name:Config39"
misc_feature /note="assembly_name:Config40"
105182. 110628
110729. 118730
/note="assembly_name:Config41"
misc_feature /note="assembly_name:Config42"
118831. 126388
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Query Match	26.4%	Score 185.2	DB 77	length 199702
Best Local Similarity	64.0%	Pred. No. 1.7e-34		
Matches 362	Conservative	0	Mismatches 193	Indels 11
				Gaps
QY 10	aagtgagaaacacgagggaacacttaaccacaacataataatagaagaacagctccctc	69		
Db 190993	AAAAAGCACAGAGGAGGTCACTCACCAAAAACGCGGAATTAAGTCAAAAGTTACTACT	191052		
QY 70	tgaccattctbagaagaagaagttcagcatcccttgytaagccactbagaagaagaat	129		
Db 191053	TGACAGATCCACAGAGAGAGAGGTGCATCATGTGCTTGGAACACCAATGGAAGGGGAGT	191112		
QY 130	tctctgggaaaaagacacattcaaccaatgaaatggaagccaaagaagaagtgaagatcta	189		
Db 191113	CATPAGG--CATTTCCCAACACAGCGGTGAAGAAATAMAGGGAGACAAAATGAGGGACTTG	191170		
QY 190	tgtagcaaaatgtaactbgaatccaaagtggttacctaggtgggtttccaatbgygaact	249		
Db 191171	TAGGCTGAAGCTTTATTTGCGGTCGA-GGTATCTATCTAAGGTGGGCTTTCCATTGGGAATT	191229		
QY 250	gtaattggaaggttaatgcaagaagacacaagtcacatbagaagacattctgagacgaan	309		
Db 191230	GTAACGTGTTGATTTACAGCAGAGTGGATCAAGTTCATTCATCGATCACACTGTGACTAAAA	191289		

Oy 310 gagagtcaccttggcatalatcgca--cagatctgcatca;tattcaagcccaatgagc 367
 |||||
 Db 191290 GGTGTTGCTCTTGCCATTATCTGCATTTGTGCATGTAGAGAG; GAGNGCAGATTAGGTAACT 191349
 |||||
 Oy 368 tgatctcagtgtgtccctalaagtggtgttaccagaagagca;tgtgtaagtaa----aaatc 422
 |||||
 Db 191350 TGTATCTAGCTGTCTCATATAGGGCAATGGTCACTAGGAAGTGGTTATATTAGGAGAGATCT 191409
 |||||
 Oy 423 ctgacttgaccacttggaggaaatggaaggagggtgagaal.tttcaacoggtgtaagtgtt 482
 |||||
 Db 191410 TGGATTGACTACTTTGGAGAACTGGGAGAGGCGAGAACTGGCAAAATTGTGTCAAGAGATG 191469
 |||||
 Oy 483 actaagacctgtcttcgtglatg. gaaatctcaacttata.ttttaatgctaaagccagaca 541
 |||||
 Db 191470 ACTAAGCCCTCTACTGATATAGAGAAATTAACTCTCATATTTAAAAATGAGATCGTAGGCA 191529
 |||||
 Oy 542 acataaataatataagaatttaccaca 567
 |||||
 Db 191530 ACATPAACCTGTATGAANTTACAACA 191555

RESULT	5
AC016665/c	
LOCUS	AC016665 151628 bp DNA 12-MAR-2000
DEFINITION	Homo sapiens clone RP11-5G23. WORKING DRAFT SEQUENCE, 3 unordered pieces.
ACCESSION	AC016665
VERSION	AC016665.2 GI:7230027
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE
1 (bases 1 to 151628)	Bliren,B., Linton,L., Nusbaum,C. and Lander,E.	Homo sapiens, clone RP11-5G33	Unpublished	
2 (bases 1 to 151628)	Bliren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.			

TITLE	Direct Submission
JOURNAL	Submitted (04-DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Mar 12, 2000 this sequence version replaced gi:5524221.

```

http://ftp.genome.washington.edu/RN/RseqMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 12854
Center clone name: 5_G_23
----- Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960721
Consensus quality: 139851 bases at least Q40
Consensus quality: 147726 bases at least Q30

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* runs of N, but the exact si

* runs of N , but the exact sizes of the gaps are unknown.

*	11707	11706:	contfg of 11706	bp in length
*	11707	11706:	gap of	100 bp
*	11807	68155:	contfg of 56349	bp in length
*	18156	68255:	gap of	100 bp
*	68256	74344:	contfg of 6089	bp in length
*	74425	74444:	gap of	100 bp
*	74445	129966:	contfg of 5552	bp in length
*	129667	130067:	gap of	100 bp
*	130067	159930:	contfg of 29864	bp in length

1. 15993

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                  /db_xref="taxon:9606"  
                  /chromosome="9"  
                  /clone="RP11-57f11"  
                  /clone_lib="RPC11.1.1"  
1. 11706  
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fragment_chain:1  
clone_end:SP6  
vector_side:left"  
11807. 68155  
misc.feature      /note="assembly_fragment:00259  
fragment_chain:1"  
68256. 74344  
misc.feature      /note="assembly_fragment:01621  
fragment_chain:1"  
74445. 129966  
misc.feature      /note="assembly_fragment:00739  
fragment_chain:2"  
130067. 159930  
misc.feature      /note="assembly_fragment:00031  
fragment_chain:2  
clone_end:T7  
vector_side:right"  
BASE COUNT      43953 a 33498 c 33745 g 48322 t 412 others  
ORIGIN
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Query Match	Similarity	Score	NO. 8:	DB 78:	Length	159930:
Best Local	Similarity	64.0%:	Pred.	10.1,9e-33:		
Matches	374:	Conservative	0:	Mismatches	192:	Indels 18: Gaps
QY 1	gltgtgtcgaagtgcgaacacatgggagaaactaaccaacacataaataacagaac	60				
Db 4114	GTGTCTATTCAGCTGAGACACAAAGAAAGTAATTCNAACAA-ACATGAATATTAACACAGC	4056				
QY 61	agtc-tctttgaccatttctagaaaaaagtttaagatcccttgtaagccactaga	119				
Db 4055	AGTATATTACTTTCAGATCCAGACAGAGACAGCAGCTGCCATGGGGCCAAACAGCA	3996				
QY 120	agaagaaaattcttcgaggaaagacacatccaaccaatgaatgagacagaagaagat	179				
Db 3995	AGTAGGGAGCATATTGGGCGCTGATCATTCAATCAGCAGGCAAGGACGAAGAGAGAT	3936				
QY 180	gaggagactatgctgcacaaaatgtaactcggatccagggtgtacctagtggtttcca	239				
Db 3935	GAGGAACCCATGGGCTGAAGACTTTATTGGGGCTCTAGGGCATTTATCCAGGCGATTTCCC	3876				
QY 240	atgggaaccttaacttgtagtttaactgaacagcagcgccaaagccatcgaggagattc	299				
Db 3875	TTGGGAACCTTCTAATTAACTAGTGGTTTAAAGAGAAAGTATGATAC-AAGTACATGAATACTGCT	3817				
QY 300	gagactgaagaatagtcactctgycatacttgc-----cgaactcgtacgtga	350				
Db 3816	GTGACTGGAAGTGGTCACTGCGCATATTCGCACATCATGTCAGTACGGGGTTCAGCA	3757				
QY 351	ctcaagcccgaatggcgtgatctcagttgtcctataaggttgtttaccaggagcagtg	410				
Db 3756	AGCTGACGTCAAGTACGTTGTATCTAGCTGTGATAGGAGGAGTGCTCACCAAGACACT	3697				

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Oy 411 t--aaagtaaaacttgcctgacacatgagaa--aaagaggtggaatttt 465
Db 3636 CGTATTAAGCAGATATCTCGATCAACCCACACGAGAAC--CGATGAGAGTAGAGAACG 3637
Oy 466 aaacggtgcagtggttgaactaagaccgtcttcgtglatg--aaatcaacttatttt 524
Db 3636 AAGCTGTGTCAAGGTGATCAAGCCCTGTGTTCCATATGCA--AAATTAACAACCTGTGTCA 3577
Oy 525 aaatgcatagcacagacacataaattataagaattacc--aa 568
Db 3576 AAATGATGCTGAGGCAACATTAATTTAGAAATCACT--ATA 3533

RESULT 9
HS424L16
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
JOURNAL
COMMENT

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repeat_region 2716..2881
/note="AluSc repeat: matches 1..109 of consensus"
misc_feature complement(3169..3588)
/note="match: GSS: Em:AQ210672"
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/note="MIR repeat: matches 2..92 of consensus"
repeat_region 5356..5502
/note="MER5B repeat: matches 3..178 of consensus"
repeat_region 5729..5917
/note="L2 repeat: matches 2533..2728 of consensus"
repeat_region 7136..7236
/note="MIR repeat: matches 46..172 of consensus"
repeat_region 8195..8495
/note="L1PA15 repeat: matches 5057..5357 of consensus"
repeat_region 8494..9287
/note="L1PA15 repeat: matches 5362..6155 of consensus"
repeat_region 9299..9439
/note="FLAM_A repeat: matches 17..116 of consensus"
repeat_region 9583..9700
/note="L2 repeat: matches 2626..2735 of consensus"
repeat_region 9874..10101
/note="L2 repeat: matches 2478..2706 of consensus"
repeat_region 10334..10369
/note="L18 copies 2 mer ca 100% conserved"
repeat_region 12720..13007
/note="AluY repeat: matches 1..311 of consensus"
repeat_region 13803..13923
/note="MSTC repeat: matches 291..405 of consensus"
repeat_region 13924..14203
/note="AluSg repeat: matches 1..286 of consensus"
repeat_region 14204..14467
/note="MSTC repeat: matches 3..291 of consensus"
repeat_region 14475..16120
/note="MSTC-internal repeat: matches 5..1574 of consensus"
repeat_region 16128..16486
/note="MSTC repeat: matches 3..403 of consensus"
repeat_region 16558..16779
/note="MIR repeat: matches 34..262 of consensus"
repeat_region 17174..17705
/note="MER67D repeat: matches 1..514 of consensus"
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repeat_region 22403..22599
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/note="L1MA8 repeat: matches 5622..6291 of consensus"
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repeat_region 25208..25325
/note="MIR repeat: matches 125..262 of consensus"
repeat_region 26113..26260
/note="MIR repeat: matches 33..195 of consensus"
repeat_region 26385..27037
/note="L1ME1 repeat: matches 5513..6168 of consensus"
repeat_region 27902..28118
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repeat_region 28119..28458
/note="AluJo repeat: matches 1..309 of consensus"
repeat_region 28982..29088
/note="L2 repeat: matches 2640..2750 of consensus"
repeat_region 29420..29627
/note="MIR repeat: matches 161..447 of consensus"
repeat_region 29628..29937
/note="AluSx repeat: matches 3..310 of consensus"
repeat_region 29938..30035
/note="MIR repeat: matches 69..161 of consensus"
repeat_region 31367..31823
/note="L1ME2 repeat: matches 5702..6155 of consensus"
repeat_region 31824..32117
/note="AluSx repeat: matches 1..294 of consensus"
repeat_region 32118..32211
/note="L1ME2 repeat: matches 5609..5702 of consensus"
repeat_region 32215..32280
/note="L1M4 repeat: matches 5236..5298 of consensus"
repeat_region 32333..32444
/note="L1M4 repeat: matches 5127..5244 of consensus"
repeat_region 33471..33644
/note="MER5B repeat: matches 2..178 of consensus"
repeat_region 34689..34787
/note="MIR repeat: matches 158..262 of consensus"
repeat_region 39859..40043
/note="MIR repeat: matches 11..195 of consensus"
repeat_region 40543..41568
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repeat_region 43171..43471
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repeat_region 43738..44056
/note="AluYb8 repeat: matches 1..306 of consensus"
repeat_region 44307..44813
/note="match: GSS: Em:B89045"
repeat_region 44795
/note="match: GSS: Em:AQ009836"
misc_feature complement(45879..46177)
/note="match: GSS: Em:B72371"
repeat_region 46178..46486
/note="AluSx repeat: matches 1..309 of consensus"
repeat_region 47808..48209
/note="L2 repeat: matches 1826..2191 of consensus"
repeat_region 48210..48552
/note="THEIR repeat: matches 1..364 of consensus"
repeat_region 48553..49095
/note="L2 repeat: matches 1162..1826 of consensus"
repeat_region 49564..49856
/note="AluSg repeat: matches 1..301 of consensus"
repeat_region 50011..50901
/note="MER54A repeat: matches 3..902 of consensus"
repeat_region 50902..50979
/note="L2 repeat: matches 1162..1826 of consensus"
repeat_region 51607..51700
/note="L1P1 repeat: matches 6060..6151 of consensus"
repeat_region 51917..52023
/note="MER1 repeat: matches 1..107 of consensus"
repeat_region 52226..53427
/note="L1MB6 repeat: matches 4969..6167 of consensus"
repeat_region 54034..54687
/note="L2 repeat: matches 2003..2750 of consensus"
repeat_region 55851..55884
/note="L17 copies 2 mer tg 82% conserved"
repeat_region 57842..57986
/note="MIR repeat: matches 7..234 of consensus"
repeat_region 59174..59318
/note="L2 repeat: matches 1823..1966 of consensus"
repeat_region 61376..61471
/note="L2 repeat: matches 1823..1966 of consensus"
repeat_region 61556..61645
/note="L2 repeat: matches 2234..2316 of consensus"
repeat_region 61646..61754
/note="MER63B repeat: matches 328..436 of consensus"
repeat_region 61755..62058
/note="AluJo repeat: matches 3..300 of consensus"
repeat_region 62059..62387
/note="MER63B repeat: matches 1..328 of consensus"
repeat_region 62388..62479
/note="L2 repeat: matches 2316..2409 of consensus"
repeat_region 62480..62911
/note="match: GSS: Em:AQ039222"
repeat_region 62652..62814
/note="MER53 repeat: matches 1..168 of consensus"
repeat_region 62831..62866
/note="L18 copies 2 mer tt 80% conserved"
repeat_region 63054..63374
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Query Match 25.8% Score 180.6; DB 92; Length 107484;
Best Local Similarity 64.7%; Pred. No. 2; le-33;

	Query Match	25.6%	Score 179.4	DB 64	Length 15038	
	Best Local Similarity	63.4%	Pred. No. 4.2e-33			
	Matches 381; Conservative	0;	Mismatches 196;	Indels 24;	Gaps 6	
OY	1 gttgtgctcaagtgaagaacatcagggagaacttaaccacaacataatacagaaac	60				
Dd	10869 gtgtcagtcagtgtagcacacagagacagacaaacttccaaaacacmtgaaattacacgaac	10810				
OY	61 agctctctt-tgaaccttctaagagaaaggltcaagcatcccttgtlaagccactlaga	119				
Dd	10809 agttattattactttacagatttccattacagaagagcgagcacccttccacagagcccattgsga	10750				
OY	120 agaagaanaattctcgcgggaaaaagcscattcaaccatgaattgagaaaccaagaaga----	175				
Dd	10749 ag-gggaaagcttttcagacacatcacactttaaccagtgattatggcgaaagagaggttg	10691				

```

Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information -----
Center project name: BA433N2
----- Summary Statistics -----
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 177465 bases at least Q40
Consensus quality: 178017 bases at least Q30
Consensus quality: 178318 bases at least Q20
Insert size: 178548; sum-of-ctrls
Insert size: 164015; 15.0% error; agarose-gel
Quality coverage: 6.31x in Q20 bases; sum-of-ctrls
Quality coverage: 6.92x in Q20 bases; agarose-gel

```

OY	1	gtgtctgcgaagttagagaaataatgaggaaacttaaaccaacataataataagaagac	60
Db	118439	GTGTTGGCTAGTTTAGACGCCAGAGAGGCAACTCATAACAAAACGGCTTAATTAACAGAAC	118496
OY	61	agcttcctttgaaccatttcttagagaaaagtgatcagcalcccttgytaaagccatagaa	120
Db	118499	AGTATTATTACTTGACAGATC-AGAAGAGAAAGGGGCAGCATCGCTCACAGGGCCAAAGGGGAAA	118557
OY	121	gaagaaaatctctcgggaaaaagaccatccaatgaatggagagaccagaagaagatg	180
Db	118558	GTCGGGAGCTGTCCAGGACACACACTCAACCAGTAGTGGGAGCACAAGACAGAAAG	118617
OY	181	agggaatcatgtgccaaaatgttaacttggatbccagggtgttaacctagttggttccaa	240
Db	118618	AGGGACCTGTGGACTGGAAGCTTTACTGTGTGGTTCAGGGCATTAACCCATGACAGGTTTTCCA	118677
OY	241	tggggaactgtgaattgttagttaatgaagaagcagaacaagtccatatggagatctig	300
Db	118678	TGGGAGATTCTCAACTGCTGGATTTTGGACAAAGCCAGCANCAATTCCTATGGGCTATCTT	118737
OY	301	agactigaagaatlaglcaacttgycatactgcacagaatctgatcacgtg-----	349
Db	118738	TGAGGAGAGAGATGTGTCCTCGACGATCTGTGTGCAGTCCATATGTGGTGTGGGGGTCAGT	118797
OY	350	attcaagcccgaagtcaggctatcatctatgttccataggttgtgttaccaaagacagt	409
Db	118798	GGGGCAGCTCCGGTAGTGGTTGCATTTAAGTGTGCTATGTGGAGGTGGTTCACCGAGAGGGGA	118857
OY	410	glaagtaa----aaalcctactgaacaacatltgaggaanaatlygaagyagtlgysaagatt	464
Db	118858	TTTGCAAGACAGATATCTGGATTGACCATATTAAAGAACATGGGMAAAGCAGAGAACTG	118917
OY	465	taaacggtgtcagtggttgactaaagacctgtctctgtgatatlgynaataatcaactatatt	524
Db	118918	AAAAATTATGTCAAGAGTACCAACTCACTTGTGTGATTCAGAAAATTTTAAACCTA--TTA	118974

Center:	Washington University Genome Sequencing Center
Center code:	WUSGC
Web site:	http://genome.wustl.edu/gsc/index.shtml
Project Information	
Center project name:	H.NH0586M15
Summary Statistics	
Sequencing vector:	M13; 100%
Sequencing vector:	plasmid; 0%
Chemistry:	Dye-terminator ET; 100% of reads
Chemistry:	Dye-terminator Big Dye; 0% of reads
Assembly program:	Phrap; version 0.990319
Consensus quality:	159025 bases at least Q40
Consensus quality:	161851 bases at least Q30
Consensus quality:	163189 bases at least Q20
Insert size:	177000; agarose-fp
Insert size:	166844; sum-of-coverage
Quality coverage:	4.10 in Q20 bases; agarose-fp
Quality coverage:	4.42 in Q20 bases; sum-of-coverage
* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.	
1	1595: contig of 1595 bp in length
1596	1695: gap of unknown length
1696	3110: contig of 1415 bp in length
3111	3210: gap of unknown length
3211	6070: contig of 2860 bp in length
6071	6170: gap of unknown length
6171	8472: contig of 2302 bp in length
8473	8572: gap of unknown length
8573	12860: contig of 4288 bp in length
12861	12960: gap of unknown length
12961	18768: contig of 5818 bp in length
18779	18878: gap of unknown length
18879	26044: contig of 7066 bp in length
25945	26044: gap of unknown length
26045	34276: contig of 8232 bp in length
34277	34376: gap of unknown length

* 34377 45419: contig of 11043 bp in length
* 45420 45519: gap of unknown length
* 61930 61930: contig of 16411 bp in length
* 61931 62030: gap of unknown length
* 62031 76275: contig of 14245 bp in length
* 76276 76375: gap of unknown length
* 76376 113122: contig of 36747 bp in length
* 113123 113223: gap of unknown length
* 113223 168041: contig of 54819 bp in length.
FEATURES
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1. 168041
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/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-586M15"
1. 1595
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1696..3110
misc_feature
/note="assembly_name:Contig5"
3211..6070
misc_feature
/note="assembly_name:Contig6"
6171..8472
misc_feature
/note="assembly_name:Contig7"
8573..12860
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18879..25944
misc_feature
/note="assembly_name:Contig10"
26045..34276
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34377..45419
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45520..61930
misc_feature
/note="assembly_name:Contig13"
62031..76275
misc_feature
/note="assembly_name:Contig14"
76376..113122
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113223..168041
misc_feature
/note="assembly_name:Contig16"

BASE COUNT 51949 a 31023 c 30835 g 53030 t 1204 others
ORIGIN

Query Match 25.3% Score 177.2; DB 75; Length 168041;
Best Local Similarity 64.8%; Pred. No. 1.4e-32;
Matches 380; Conservative 0; Mismatches 183; Indels 23; Gaps 7;
OY 1 gttgtgtaagtgagaaacatgagaaacttaacccaataaataaagaac 60
DB 112532 GTCCGGGTGAGTGAACACAGAGAGCGCACAGCAAAACATGAACTAACAGAAC 112591
OY 61 agtctcttgaccattcttaagaaagagttcaagatcccttgtaaggccaactagaa 120
DB 112592 AGTATTGCTT-ACAAATTCACAGACAGAGGCGCAGACCTCGTAGAGCTATGGGA 112650
OY 121 gaagaataatctctgagaaagacacattcaac-caatgaatgagagcaagaagaagagt 179
DB 112651 AGGGAAGCTGCTGTGACATGTGACGCCCAACCGAAGGTGAGAGCAAGAGAAAGC 112710
OY 180 gaagagatcatgtgccaataatgtaactgagatcgaaggtgttaacttagtgggtttca 239
DB 112711 GAGAGACTATGAGCGCAGAGGCTTTATTGGATCCAGGGGTGTCACCCACAAAGTTTCT 112770
OY 240 atgggaactgtaattgtgagtttaatgcaagcagcacaagttccatggaagcattct 299
DB 112771 TTGGACAGTTCTAAATTGTGATTTAGACCAACAGCAGAGGCTCCATGGACTACGCT 112830

OY 300 gagactgaagatagtcacttggcatatctgcacagaatgatcatgt----- 349
DB 112831 GTAACGTAGGGGTGGTCACTGCAGCCTATCTGTCACTGCAATTCAGAGGTGTGGGGTCAA 112890
OY 350 -attcaagcccaagtagtgctgtatctagttgttccataa----tggtaccagagagca 405
DB 112891 TGGGCAAGTCGATATAGGTGTGTATCTAGCTGCCATATGATGATGTCACCGAGAGCA 112950
OY 406 gttg--gtaagtaaatctgactgaacacattgaggaatggaaggggtggaagatt 463
DB 112951 GTTTATTAAGGCAATATCTGGGTGACACACTTTAGGAAGTGGAGAGTGGAGAACT 113010
OY 464 ttaacggtgtcagttgtgactaagaccgtctctgtgta--tgaataactatatt 522
DB 113011 GGAAGCTG----AAGGTGACTTAAGCCCAAGTTCTGATTAAGAAATCCAACTATATT 113066
OY 523 ttaatgcatagccagacaacataaataataagaatttcacaa 568
DB 113067 TAAATGATGTGTGAGGCAACATTAATTTAGAACTCA--TACAA 113112

Search completed: August 27, 2001, 18:06:14
Job time: 9447 sec

